

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 11, 2005, 18:46:16 ; Search time 27 Seconds  
(without alignments)  
28.276 Million cell updates/sec

Title: US-09-733-179A-2

Perfect score: 84

Sequence: 1 CGTQARQDPSTGPI 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 217621 seqs, 50897439 residues

Total number of hits satisfying chosen parameters: 217621

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Pending\_Patents\_AA\_New.\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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5	42	50.0	641	6	US-10-408-765-1675
6	41	48.8	300	6	US-10-857-765-8
7	41	48.8	371	6	US-10-857-765-6
8	41	48.8	424	6	US-10-732-923-1548
9	40.5	48.2	828	6	US-10-995-561-983
10	40.5	48.2	828	6	US-60-636-722-329
11	40.5	48.2	828	6	US-60-636-722-331
12	40.5	48.2	918	6	US-10-995-561-981
13	40.5	48.2	918	8	US-60-636-722-327
14	40.5	48.2	918	8	US-60-636-722-333
15	40.5	48.2	999	6	US-10-486-678-14
16	40.5	48.2	1019	6	US-10-486-678-13
17	40.5	48.2	1019	6	US-10-995-561-982
18	40.5	48.2	1019	8	US-60-636-722-326
19	40.5	48.2	1019	8	US-60-636-722-330
20	40.5	48.2	1019	8	US-60-636-722-332
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23	40	47.6	316	6	US-10-408-765-2776
24	40	47.6	348	6	US-10-871-385-13
25	40	47.6	407	7	US-11-016-106-5

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29	40	47.6	780	6	US-10-732-923-1580	Sequence 1580, Ap
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31	39	46.4	374	6	US-10-399-103A-728	Sequence 728, App
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33	39	46.4	437	1	PCT-US02-09107B-50329	Sequence 50329, A
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37	39	46.4	471	1	PCT-US04-24204-32	Sequence 32, Appl
38	39	46.4	471	6	US-10-899-557-32	Sequence 32, Appl
39	39	46.4	521	6	US-10-408-765-710	Sequence 710, App
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51	38	45.2	435	1	PCT-US02-09107B-49410	Sequence 49410, A
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53	38	45.2	1731	6	US-10-732-923-8855	Sequence 8855, Ap
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57	38	45.2	3035	6	US-10-732-923-8108	Sequence 8108, Ap
58	38	45.2	3035	6	US-10-990-328-10926	Sequence 10926, A
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64	37	44.0	273	6	US-10-983-340-30	Sequence 30, Appl
65	37	44.0	292	6	US-10-777-288A-3849	Sequence 3849, Ap
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67	37	44.0	387	6	US-10-965-898-70	Sequence 70, Appl
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77	36	42.9	86	6	US-10-220-366A-14381	Sequence 14381, A
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80	36	42.9	138	1	PCT-US02-09107B-53863	Sequence 53863, A
81	36	42.9	138	1	PCT-US02-09107B-53948	Sequence 53948, A
82	36	42.9	138	1	PCT-US02-09107B-54083	Sequence 54083, A
83	36	42.9	163	6	US-10-777-288A-2541	Sequence 2541, Ap
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92	36	42.9	328	1	PCT-US02-09107B-61804	Sequence 61804, A
93	36	42.9	392	6	US-10-399-103A-721	Sequence 721, App
94	36	42.9	407	6	US-10-408-765-2354	Sequence 2354, Ap
95	36	42.9	414	8	US-60-629-811-88	Sequence 88, Appl
96	36	42.9	417	6	US-10-940-655A-4	Sequence 4, Appli
97	36	42.9	422	7	US-10-871-385-11	Sequence 11, Appl
98	36	42.9	432	6	US-10-732-923-6030	Sequence 6030, Ap

99	36	42.9	546	6	US-10-994-151-84	Sequence 84, Appl	172	35	41.7	915	6	US-10-952-045-74	Sequence 74, Appl
100	36	42.9	546	6	US-10-994-116-84	Sequence 84, Appl	173	35	41.7	916	1	PCT-US02-09107B-65074	Sequence 65074, A
101	36	42.9	546	6	PCT-US02-09107B-68162	Sequence 18162, A	174	35	41.7	916	1	PCT-US02-09107B-65995	Sequence 65995, A
102	36	42.9	546	6	US-10-732-923-15061	Sequence 15061, A	175	35	41.7	939	1	PCT-US02-09107B-68011	Sequence 68011, A
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106	36	42.9	1038	6	US-10-481-031B-52	Sequence 52, Appl	179	35	41.7	1175	1	PCT-US02-09107B-50732	Sequence 50732, A
107	36	42.9	1141	6	US-10-990-328-12128	Sequence 12128, A	180	35	41.7	1260	1	PCT-US04-37204-5453	Sequence 5453, A
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112	35.5	42.3	523	6	US-10-732-923-871	Sequence 871, A	185	35	41.7	1511	6	US-10-482-029-123	Sequence 123, A
113	35.5	42.3	551	6	US-10-732-923-863	Sequence 863, A	186	35	41.7	1119	6	US-10-777-288A-3416	Sequence 3416, A
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115	35.5	42.3	582	1	PCT-US02-09107B-64783	Sequence 64783, A	188	34.5	41.1	557	6	US-10-955-745-92	Sequence 92, Appl
116	35.5	42.3	612	8	US-60-636-722-973	Sequence 973, A	189	34.5	41.1	557	6	US-10-955-745-93	Sequence 93, Appl
117	35.5	42.3	615	8	US-60-636-722-971	Sequence 971, A	190	34.5	41.1	557	6	US-10-955-745-178	Sequence 178, A
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119	35.5	42.3	615	8	US-60-636-722-974	Sequence 974, A	192	34.5	41.1	559	6	US-10-955-745-91	Sequence 91, Appl
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121	35.5	42.3	616	8	US-60-636-722-977	Sequence 977, A	194	34	40.5	36	6	PCT-US04-37204-6863	Sequence 6863, A
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125	35	41.7	43	6	US-10-963-903-133	Sequence 133, A	198	34	40.5	135	6	US-10-732-923-2319	Sequence 2319, A
126	35	41.7	53	7	US-10-220-366A-22535	Sequence 22535, A	199	34	40.5	143	6	US-10-732-923-2351	Sequence 2351, A
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OM protein - protein search, using sw model

Run on: January 11, 2005, 18:47:01 ; Search time 145 Seconds  
(without alignments)  
37.300 Million cell updates/sec

Title: US-09-733-179A-2

Perfect score: 84

Sequence: 1 CGTQARQGPSTGPI 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1603904 seqs, 360571292 residues

Total number of hits satisfying chosen parameters: 1603904

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	84	100.0	643	10	US-09-919-039-204
5	84	100.0	643	16	US-10-755-889-396
6	84	100.0	665	9	US-09-925-302-724
7	84	100.0	655	10	US-09-968-862-724
8	67	79.8	12	10	US-09-733-179A-3
9	46	54.8	76	17	US-10-425-115-311583
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12	45	53.6	201	16	US-10-767-701-32548
13	44.5	53.0	176	17	US-10-425-115-262575

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44	52.4	287	14	US-10-017-161-1320	Sequence 1320, Ap
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43	51.2	50	16	US-10-437-963-184270	Sequence 184270,
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43	51.2	330	9	US-09-764-898-184	Sequence 184, App
43	51.2	484	14	US-10-156-761-12068	Sequence 12068, A
43	51.2	718	16	US-10-437-963-183165	Sequence 183165,
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OM protein - protein search, using sw model

Run on: January 11, 2005, 18:45:06 ; Search time 21 Seconds  
(without alignments)

47.370 Million cell updates/sec

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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6	42	50.0	239	4	US-09-252-991A-25790
7	42	50.0	641	4	US-09-919-039-73
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13	41	48.8	272	4	US-09-270-767-44742
14	41	48.8	284	4	US-09-252-991A-32586
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76	43	51.2	312	30	US-10-438-246-8969	Sequence 8969, App	149	41	48.8	131	30	US-10-437-963-108633	Sequence 108633, A	
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81	43	51.2	317	30	US-10-437-963-183165	Sequence 183165, A	154	41	48.8	146	15	US-10-921-235-55	Sequence 55, App	
82	43	51.2	318	32	US-10-679-063-19300	Sequence 19300, A	155	41	48.8	147	14	US-09-002-485-11	Sequence 11, App	
83	43	51.2	319	26	US-10-087-192-1071	Sequence 1071, App	156	41	48.8	147	22	US-09-799-777-11	Sequence 11, App	
84	43	51.2	320	30	US-10-467-909-5	Sequence 5, App	157	41	48.8	147	22	US-10-767-701-55129	Sequence 55129, A	
85	42.5	50.6	110	23	US-09-877-843-85	Sequence 85, App	158	41	48.8	166	33	US-10-424-599-216773	Sequence 216773, A	
86	42.5	50.6	111	24	US-09-930-512-691	Sequence 69, App	159	41	48.8	184	30	US-10-437-963-196824	Sequence 196824, A	
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94	42.5	50.6	119	28	US-10-212-760-765	Sequence 765, App	167	41	48.8	284	29	US-10-366-683-32586	Sequence 32586, A	
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123	42.5	50.6	148	641	29	US-10-380-408A-7	Sequence 7, App	196	41	48.8	524	36	US-60-191-637-21149	Sequence 21149, A
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128	42.5	50.6	153	641	36	US-60-443-418-1675	Sequence 443, App	201	41	48.8	524	36	US-60-191-637-21149	Sequence 21149, A
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132	42.5	50.6	157	641	36	US-60-474-850-370	Sequence 370, App	205	41	48.8	524	36	US-60-191-637-21149	Sequence 21149, A
133	42.5	50.6	158	641	36	US-10-366-683-29274	Sequence 29274, App	206	41	48.8	524	36	US-60-191-637-21149	Sequence 21149, A
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